

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:26:10 ; Search time 78.5658 Seconds
(without alignments)
3345.152 Million cell updates/sec

Title: US-10-715-667-21

Perfect score: 3334

Sequence: 1 MNQVTIQMDAVIALYILFSW.....TYFPQNIIESHFNRIISLEK 629

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubppaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubppaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubppaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubppaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubppaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubppaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	3334	100.0	629	3	US-09-972-708-21
2	3334	100.0	629	4	US-10-105-930-10
3	3334	100.0	629	3	US-10-715-667-21
4	3314	99.4	629	3	US-09-853-180-2
5	3314	99.4	629	5	US-10-797-157-6
6	3314	99.4	629	5	US-10-720-026-2
7	3314	99.4	629	5	US-10-667-289-2
8	3314	99.4	629	5	US-10-667-290-2
9	3312	99.3	629	4	US-10-105-930-6
10	2972	89.1	565	3	US-09-972-708-23
11	2972	89.1	565	4	US-10-715-667-23
12	2278.5	68.3	644	3	US-09-972-708-27
13	2278.5	68.3	644	4	US-10-715-667-27
14	2212	66.3	428	4	US-10-105-930-8
15	2195	65.8	428	4	US-10-105-930-4
16	2037	61.1	384	3	US-09-972-708-26
17	2037	61.1	384	4	US-10-247-463-2
18	2037	61.1	384	4	US-10-715-667-26
19	2037	61.1	384	6	US-11-016-106-2
20	1888	56.6	356	3	US-09-972-708-25
21	1888	56.6	356	4	US-10-715-667-25
22	1715	51.4	337	4	US-10-105-930-2
23	1020.5	30.6	344	3	US-09-972-708-16
24	1020.5	30.6	344	4	US-10-715-667-16
25	293	8.8	52	4	US-10-105-930-24
26	262	7.9	46	4	US-10-105-930-28
27	232	7.0	951	3	US-09-313-942-9

28	232	7.0	951	3	US-09-935-868-9	Sequence 9, Appl1
29	232	7.0	951	4	US-10-287-025-9	Sequence 9, Appl1
30	232	7.0	951	4	US-10-282-162-9	Sequence 9, Appl1
31	232	7.0	951	6	US-11-134-114-9	Sequence 9, Appl1
32	227	6.8	861	4	US-10-398-666-12	Sequence 12, Appl1
33	224	6.7	39	4	US-10-105-930-27	Sequence 27, Appl1
34	222	6.7	862	3	US-09-853-180-5	Sequence 5, Appl1
35	222	6.7	862	5	US-10-797-157-7	Sequence 7, Appl1
36	222	6.7	862	5	US-10-370-715B-68	Sequence 68, Appl1
37	222	6.7	862	5	US-10-720-026-4	Sequence 4, Appl1
38	222	6.7	862	5	US-10-667-289-4	Sequence 4, Appl1
39	222	6.7	862	5	US-10-667-290-4	Sequence 4, Appl1
40	220	6.6	859	3	US-09-313-942-7	Sequence 7, Appl1
41	220	6.6	859	3	US-09-935-868-7	Sequence 7, Appl1
42	220	6.6	859	4	US-10-287-035-7	Sequence 7, Appl1
43	220	6.6	859	4	US-10-282-162-7	Sequence 7, Appl1
44	220	6.6	859	6	US-11-134-114-7	Sequence 7, Appl1
45	215	6.4	918	3	US-09-853-180-4	Sequence 4, Appl1
46	215	6.4	918	3	US-09-972-708-8	Sequence 8, Appl1
47	215	6.4	918	3	US-09-829-472A-9	Sequence 9, Appl1
48	215	6.4	918	4	US-10-177-293-230	Sequence 230, Appl1
49	215	6.4	918	4	US-10-295-027-74	Sequence 74, Appl1
50	215	6.4	918	4	US-10-058-270A-32	Sequence 32, Appl1
51	215	6.4	918	4	US-10-715-667-8	Sequence 8, Appl1
52	215	6.4	918	5	US-10-720-026-3	Sequence 3, Appl1
53	215	6.4	918	5	US-10-667-289-3	Sequence 3, Appl1
54	215	6.4	918	5	US-10-667-290-3	Sequence 3, Appl1
55	214	6.4	918	6	US-11-067-251-5	Sequence 5, Appl1
56	213	6.4	332	3	US-09-313-942-10	Sequence 10, Appl1
57	213	6.4	332	3	US-09-935-868-10	Sequence 10, Appl1
58	213	6.4	332	4	US-10-287-035-10	Sequence 10, Appl1
59	213	6.4	332	4	US-10-282-162-10	Sequence 10, Appl1
60	213	6.4	332	6	US-11-134-114-10	Sequence 10, Appl1
61	213	6.4	918	5	US-10-850-270-6	Sequence 6, Appl1
62	212	6.4	708	4	US-10-313-135-2	Sequence 2, Appl1
63	210	6.3	1158	3	US-09-313-942-26	Sequence 26, Appl1
64	210	6.3	1158	3	US-09-935-868-26	Sequence 26, Appl1
65	210	6.3	1158	4	US-10-287-035-26	Sequence 26, Appl1
66	210	6.3	1158	4	US-10-282-162-26	Sequence 26, Appl1
67	210	6.3	1158	6	US-11-134-114-26	Sequence 26, Appl1
68	210	6.3	1168	3	US-09-313-942-24	Sequence 24, Appl1
69	210	6.3	1168	3	US-09-935-868-24	Sequence 24, Appl1
70	210	6.3	1168	4	US-10-287-035-24	Sequence 24, Appl1
71	210	6.3	1168	4	US-10-282-162-24	Sequence 24, Appl1
72	210	6.3	1168	6	US-11-134-114-24	Sequence 24, Appl1
73	208	6.2	329	5	US-10-755-889-426	Sequence 426, Appl1
74	208	6.2	329	5	US-10-884-043-1	Sequence 1, Appl1
75	208	6.2	807	4	US-10-311-473-12	Sequence 12, Appl1
76	207.5	6.2	488	4	US-10-079-625-5	Sequence 5, Appl1
77	197	5.9	34	4	US-10-105-930-29	Sequence 29, Appl1
78	196	5.9	36	3	US-09-864-761-48948	Sequence 48948, A
79	194	5.8	1097	3	US-09-972-708-6	Sequence 6, Appl1
80	194	5.8	1097	4	US-10-715-667-6	Sequence 6, Appl1
81	194	5.8	1119	4	US-10-276-776-2690	Sequence 2690, Appl1
82	192.5	5.8	652	3	US-09-972-708-14	Sequence 14, Appl1
83	192.5	5.8	652	4	US-10-006-265-2	Sequence 2, Appl1
84	192.5	5.8	652	4	US-10-715-667-14	Sequence 14, Appl1
85	191.5	5.7	649	3	US-09-892-949-46	Sequence 46, Appl1
86	191.5	5.7	649	4	US-10-351-157-109	Sequence 109, Appl1
87	191.5	5.7	649	4	US-10-772-531-46	Sequence 46, Appl1
88	191.5	5.7	649	5	US-10-982-553-46	Sequence 46, Appl1
89	191.5	5.7	662	3	US-09-972-708-15	Sequence 15, Appl1
90	191.5	5.7	662	3	US-09-892-949-54	Sequence 54, Appl1
91	191.5	5.7	662	4	US-10-006-265-17	Sequence 17, Appl1
92	191.5	5.7	662	4	US-10-351-157-5	Sequence 5, Appl1
93	191.5	5.7	662	4	US-10-352-554-5	Sequence 5, Appl1
94	191.5	5.7	662	4	US-10-772-531-54	Sequence 54, Appl1
95	191.5	5.7	662	4	US-10-715-667-15	Sequence 15, Appl1
96	191.5	5.7	662	5	US-10-982-553-54	Sequence 54, Appl1
97	191.5	5.7	732	3	US-09-892-949-42	Sequence 2, Appl1
98	191.5	5.7	732	4	US-10-351-157-111	Sequence 111, Appl1
99	191.5	5.7	732	4	US-10-772-531-2	Sequence 2, Appl1
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ALIGNMENTS

RESULT 1
US-09-972-708-21
; Sequence 21, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPR1 AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: Patentin version 3.1
; SEQ ID NO 21
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-21

Query Match 100.0%; Score 3334; DB 3; Length 629;
Best Local Similarity 100.0%; Pred. No. 1.3e-242;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOAALXNQ 60
DB 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOAALXNQ 60
QY 61 PKLAFYKNGIKERQITRINKTARLWYKNFLBPHASMYCTACBCKPFOETLIGCKDIS 120
DB 61 PKLAFYKNGIKERQITRINKTARLWYKNFLBPHASMYCTACBCKPFOETLIGCKDIS 120
QY 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
QY 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
QY 181 ISTDSLQGGKYLWVQAAANALGMBESKQIHLDDIYIPSAAVISRAETINATVPKTI 240
DB 181 ISTDSLQGGKYLWVQAAANALGMBESKQIHLDDIYIPSAAVISRAETINATVPKTI 240
QY 241 YNDSQTTIEKVSCEMRKYATNTQTNVKEFDNFTYVOOSEFYLBEPNIKYVQVRCQETG 300
DB 241 YNDSQTTIEKVSCEMRKYATNTQTNVKEFDNFTYVOOSEFYLBEPNIKYVQVRCQETG 300
QY 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
DB 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
QY 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
DB 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
QY 361 IYFAVWLSILSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVYKMLQENSELMN 420
DB 361 IYFAVWLSILSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVYKMLQENSELMN 420
QY 421 NNSSEBOVLVYDPMITEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
DB 421 NNSSEBOVLVYDPMITEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
QY 481 NTGYKPOISNPLPBGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPFAFSVSVNSL 540
DB 481 NTGYKPOISNPLPBGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPFAFSVSVNSL 540
QY 541 SNTIFLGLSLILNQGECSSPDIONSVEBETTMLENDSPSSETIPBQTLLPBEFVSCIGI 600
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QY 601 VNEBLPSINTYFPQNLISHFNRIISLARK 629

DB 601 VNEBLPSINTYFPQNLISHFNRIISLARK 629

RESULT 2
US-10-105-930-10
; Sequence 10, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yaguchi, No. US20030009018A1ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105US1
; CURRENT APPLICATION NUMBER: US/10/105,930
; PRIOR FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 629
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-10

Query Match 100.0%; Score 3334; DB 4; Length 629;
Best Local Similarity 100.0%; Pred. No. 1.3e-242;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOAALXNQ 60
DB 1 MNQVITQMDAVIALYILFSWCHGGITNINCSGHIWVEBATTFKMGMINISYCOAALXNQ 60
QY 61 PKLAFYKNGIKERQITRINKTARLWYKNFLBPHASMYCTACBCKPFOETLIGCKDIS 120
DB 61 PKLAFYKNGIKERQITRINKTARLWYKNFLBPHASMYCTACBCKPFOETLIGCKDIS 120
QY 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
QY 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVTCVLEYSGNMTCTWNAKLTYYIDTKYVHVAKSLTEBEOQYLTSSYIN 180
QY 181 ISTDSLQGGKYLWVQAAANALGMBESKQIHLDDIYIPSAAVISRAETINATVPKTI 240
DB 181 ISTDSLQGGKYLWVQAAANALGMBESKQIHLDDIYIPSAAVISRAETINATVPKTI 240
QY 241 YNDSQTTIEKVSCEMRKYATNTQTNVKEFDNFTYVOOSEFYLBEPNIKYVQVRCQETG 300
DB 241 YNDSQTTIEKVSCEMRKYATNTQTNVKEFDNFTYVOOSEFYLBEPNIKYVQVRCQETG 300
QY 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
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QY 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
DB 301 KRYWQPMWSLFPFKTPEVTPQVTSKAFQHDITWNSGLTVASISTGHLTSDNRGDIGLLGM 360
QY 361 IYFAVWLSILSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVYKMLQENSELMN 420
DB 361 IYFAVWLSILSLIGIFNRSFRGTGIRKRIILLIPKMLYEDI PMKKSNNVYKMLQENSELMN 420
QY 421 NNSSEBOVLVYDPMITEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
DB 421 NNSSEBOVLVYDPMITEIKEIFIPEHKPTDYKKENTGPLETRDY PONSLEPNTTVYYIPDL 480
QY 481 NTGYKPOISNPLPBGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPFAFSVSVNSL 540
DB 481 NTGYKPOISNPLPBGSHLSNNNEITSLLTKPVDSDSGNNPRLQKHPFAFSVSVNSL 540
QY 541 SNTIFLGLSLILNQGECSSPDIONSVEBETTMLENDSPSSETIPBQTLLPBEFVSCIGI 600
DB 541 SNTIFLGLSLILNQGECSSPDIONSVEBETTMLENDSPSSETIPBQTLLPBEFVSCIGI 600

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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:26:10 ; Search time 44.4665 Seconds
(without alignment)

3345.152 Million cell updates/sec

Title: US-10-715-667-25

Perfect score: 1934
Sequence: 1 MNQVTIQMDVIALYILFSW.....TVASISGHTLSGLKEGSGYC 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1867569 seqs, 417829326 residues

Total number of hits satisfying chosen parameters: 1867569

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

Database : Published Applications AA Main:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US10A_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US10B_PUBCOMB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US11_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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1	1934	100.0	356	3	US-09-972-708-25
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3	1888	97.6	428	4	US-10-105-930-8
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5	1888	97.6	629	4	US-10-105-930-10
6	1888	97.6	629	4	US-10-715-667-21
7	1881	97.3	384	4	US-09-972-708-26
8	1881	97.3	384	4	US-10-247-463-2
9	1881	97.3	384	4	US-10-715-667-26
10	1881	97.3	428	6	US-11-016-106-2
11	1871	96.7	428	4	US-10-105-930-4
12	1871	96.7	629	4	US-10-105-930-6
13	1868	96.6	629	4	US-09-853-180-2
14	1868	96.6	629	5	US-10-720-026-2
15	1868	96.6	629	5	US-10-720-026-2
16	1868	96.6	629	5	US-10-667-289-2
17	1868	96.6	629	5	US-10-667-289-2
18	1732	89.6	565	3	US-09-972-708-23
19	1732	89.6	565	4	US-10-715-667-23
20	1715	89.6	337	4	US-10-105-930-2
21	1417.5	73.3	644	3	US-09-972-708-27
22	1417.5	73.3	644	4	US-10-715-667-27
23	1020.5	52.8	344	4	US-09-972-708-16
24	1020.5	52.8	344	4	US-10-715-667-16
25	293	15.1	52	4	US-10-105-930-24
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27	227	11.7	861	4	US-10-398-666-12

28	224	11.6	39	4	US-10-105-930-27	Sequence 27, Appl
29	222	11.5	862	3	US-09-853-180-5	Sequence 5, Appl
30	222	11.5	862	5	US-10-797-157-7	Sequence 7, Appl
31	222	11.5	862	5	US-10-370-715B-68	Sequence 68, Appl
32	222	11.5	862	5	US-10-720-026-4	Sequence 4, Appl
33	222	11.5	862	5	US-10-667-289-4	Sequence 4, Appl
34	222	11.5	862	5	US-10-667-290-4	Sequence 4, Appl
35	215.5	11.1	859	3	US-09-313-942-7	Sequence 7, Appl
36	215.5	11.1	859	3	US-09-313-942-7	Sequence 7, Appl
37	215.5	11.1	859	4	US-10-287-035-7	Sequence 7, Appl
38	215.5	11.1	859	4	US-10-282-162-7	Sequence 7, Appl
39	215.5	11.1	859	6	US-11-134-114-7	Sequence 7, Appl
40	215.5	11.1	951	3	US-09-313-942-9	Sequence 9, Appl
41	215.5	11.1	951	3	US-09-313-868-9	Sequence 9, Appl
42	215.5	11.1	951	4	US-10-287-035-9	Sequence 9, Appl
43	215.5	11.1	951	4	US-10-282-162-9	Sequence 9, Appl
44	215.5	11.1	951	6	US-11-134-114-9	Sequence 9, Appl
45	213	11.0	332	3	US-09-313-942-10	Sequence 10, Appl
46	213	11.0	332	3	US-09-935-868-10	Sequence 10, Appl
47	213	11.0	332	4	US-10-287-035-10	Sequence 10, Appl
48	213	11.0	332	6	US-11-134-114-10	Sequence 10, Appl
49	213	11.0	332	6	US-09-853-180-4	Sequence 4, Appl
50	212.5	11.0	918	3	US-10-715-667-8	Sequence 8, Appl
51	212.5	11.0	918	3	US-10-720-026-3	Sequence 3, Appl
52	212.5	11.0	918	3	US-10-850-270-6	Sequence 6, Appl
53	212.5	11.0	918	4	US-10-177-293-230	Sequence 230, Appl
54	212.5	11.0	918	4	US-10-295-027-74	Sequence 74, Appl
55	212.5	11.0	918	4	US-10-058-270A-32	Sequence 32, Appl
56	212.5	11.0	918	4	US-10-715-667-8	Sequence 8, Appl
57	212.5	11.0	918	5	US-10-720-026-3	Sequence 3, Appl
58	212.5	11.0	918	5	US-10-850-270-6	Sequence 6, Appl
59	212.5	11.0	918	5	US-10-667-289-3	Sequence 3, Appl
60	212.5	11.0	918	5	US-10-667-290-3	Sequence 3, Appl
61	211.5	10.9	708	4	US-10-313-135-2	Sequence 2, Appl
62	211.5	10.9	918	6	US-11-067-251-5	Sequence 5, Appl
63	208	10.8	329	4	US-10-755-889-426	Sequence 426, Appl
64	208	10.8	329	5	US-10-884-043-1	Sequence 1, Appl
65	207.5	10.7	488	4	US-10-079-625-5	Sequence 5, Appl
66	207.5	10.7	807	4	US-10-311-473-12	Sequence 12, Appl
67	207.5	10.7	1158	3	US-09-313-942-26	Sequence 26, Appl
68	207.5	10.7	1158	4	US-09-935-868-26	Sequence 26, Appl
69	207.5	10.7	1158	4	US-10-287-035-26	Sequence 26, Appl
70	207.5	10.7	1158	4	US-10-282-162-26	Sequence 26, Appl
71	207.5	10.7	1158	6	US-11-134-114-26	Sequence 26, Appl
72	207.5	10.7	1168	3	US-09-313-942-24	Sequence 24, Appl
73	207.5	10.7	1168	3	US-09-935-868-24	Sequence 24, Appl
74	207.5	10.7	1168	4	US-10-287-035-24	Sequence 24, Appl
75	207.5	10.7	1168	4	US-10-282-162-24	Sequence 24, Appl
76	207.5	10.7	1168	6	US-11-134-114-24	Sequence 24, Appl
77	197	10.2	34	4	US-10-105-930-29	Sequence 29, Appl
78	196	10.1	36	3	US-10-105-930-29	Sequence 29, Appl
79	186.5	9.6	837	3	US-09-864-761-48948	Sequence 48948, A
80	186.5	9.6	837	5	US-10-659-229-35	Sequence 35, Appl
81	182	9.4	1097	3	US-10-880-101A-35	Sequence 35, Appl
82	182	9.4	1097	3	US-09-972-708-6	Sequence 6, Appl
83	182	9.4	1119	4	US-10-715-667-6	Sequence 6, Appl
84	170	8.8	836	4	US-10-276-774-2690	Sequence 2690, Appl
85	170	8.8	836	4	US-09-972-708-9	Sequence 9, Appl
86	170	8.8	836	4	US-10-659-229-34	Sequence 34, Appl
87	170	8.8	836	4	US-10-715-667-9	Sequence 9, Appl
88	167.5	8.7	603	5	US-10-880-101A-34	Sequence 34, Appl
89	167	8.6	385	4	US-10-071-962-27	Sequence 27, Appl
90	167	8.6	405	3	US-09-880-578-19	Sequence 19, Appl
91	167	8.6	405	4	US-09-736-842-2	Sequence 2, Appl
92	167	8.6	413	3	US-10-074-901-2	Sequence 2, Appl
93	167	8.6	425	3	US-09-037-657-13	Sequence 13, Appl
94	167	8.6	425	3	US-09-880-578-6	Sequence 6, Appl
95	163.5	8.5	303	3	US-09-037-657-15	Sequence 15, Appl
96	163.5	8.5	389	3	US-09-880-578-21	Sequence 21, Appl
97	163.5	8.5	389	3	US-09-880-578-27	Sequence 27, Appl
98	163.5	8.5	389	3	US-09-880-578-29	Sequence 29, Appl
99	163.5	8.5	422	3	US-09-880-578-2	Sequence 2, Appl
100	163	8.4	407	4	US-10-247-463-5	Sequence 5, Appl

ALIGNMENTS

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RESULT 1
US-09-972-708-25
; Sequence 25, Application US/09972708
; Publication No. US20030059871A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/09/972,708
; CURRENT FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-972-708-25
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Best Local Similarity 100.0%; Pred. No. 3.8e-157;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 121 SGYPDIPDEVTCVYIYSGNMCTWNAAGKLTIIDTKYVHVKSLETBEOQYLTSSYIN 180
QY 181 ISTSLQGGKKYLVWVOAANALGMEESKQLOIHDDIYIPSAVTSRAETINATVPKTI 240
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DB 241 YMDSQTTIEKYSCEMRKYATNTQTNVKEFDTNFTYVOOSEFYLEPNIKYVFOVRCQETG 300
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RESULT 2
US-10-715-667-25
; Sequence 25, Application US/10715667
; Publication No. US20040152161A1
; GENERAL INFORMATION:
; APPLICANT: Immunex Corporation
; APPLICANT: Cosman, David J.
; APPLICANT: Mosley, Bruce A.
; APPLICANT: Bird, Timothy A.
; APPLICANT: Dubose, Robert F.
; APPLICANT: Wiley, Steven R.
; TITLE OF INVENTION: HEMATOPOIETIN RECEPTORS HPRI AND HPR2
; FILE REFERENCE: 3160-B
; CURRENT APPLICATION NUMBER: US/10/715,667
; CURRENT FILING DATE: 2003-11-14
; PRIOR APPLICATION NUMBER: US/09/972,708
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; PRIOR FILING DATE: 2001-10-05
; NUMBER OF SEQ ID NOS: 29
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 25
; LENGTH: 356
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-715-667-25
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Best Local Similarity 100.0%; Pred. No. 3.8e-157;
Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 PRKLHFYKNGIKERFOITRIKNTARLWYKNFLBPHASMYCTACBPKHFOETLLCGKD 120
QY 121 SGYPDIPDEVTCVYIYSGNMCTWNAAGKLTIIDTKYVHVKSLETBEOQYLTSSYIN 180
DB 121 SGYPDIPDEVTCVYIYSGNMCTWNAAGKLTIIDTKYVHVKSLETBEOQYLTSSYIN 180
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DB 241 YMDSQTTIEKYSCEMRKYATNTQTNVKEFDTNFTYVOOSEFYLEPNIKYVFOVRCQETG 300
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RESULT 3
US-10-105-930-8
; Sequence 8, Application US/10105930
; Publication No. US20030009018A1
; GENERAL INFORMATION:
; APPLICANT: Maeda, Masatsugu
; APPLICANT: Yasuchi, No. US20030009018A1:ko
; TITLE OF INVENTION: NOVEL HEMOPOIETIN RECEPTOR PROTEIN, NR12
; FILE REFERENCE: 06501-105051
; CURRENT APPLICATION NUMBER: US/10/105,930
; CURRENT FILING DATE: 2002-03-25
; PRIOR APPLICATION NUMBER: PCT/JP00/06654
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: JP 2000-240397
; PRIOR FILING DATE: 2000-08-03
; PRIOR APPLICATION NUMBER: JP 11-273358
; PRIOR FILING DATE: 1999-09-27
; NUMBER OF SEQ ID NOS: 77
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 8
; LENGTH: 428
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-105-930-8
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AC OSVWKS;
DT 01-FEB-2005 (TREMBLrel. 29, Created)
DT 01-FEB-2005 (TREMBLrel. 29, Last sequence update)
DT 13-SEP-2005 (TREMBLrel. 31, Last annotation update)
DE Interleukin 23 receptor
GN Name=IL23R; ORFName=RP11-131015.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall R.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RA Davidson C.;
RL Submitted (MAY-2005) to the EMBL/Genbank/DBJ databases.
DR EMBL; AL389925; CAH70406.1; -; Genomic DNA.
DR EMBL; AL109843; CAI22678.1; -; Genomic DNA.
DR EMBL; AL109843; CAH70406.1; JOINED; Genomic DNA.
DR EMBL; AL389925; CAI22678.1; JOINED; Genomic DNA.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0016021; C:Integral to membrane, IEA.
DR GO; GO:0004872; F:Receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR PROSITE; PS50853; FN3; 2.
DR Receptor; Repeat; Transmembrane.
SQ SEQUENCE 629 AA; 7172 MW; AC63C89B81ABF05 CRC64;

Query Match 100.0%; Score 3334; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 5,76-212;
Matches 629; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNQVTTQMDAVIALYILFSWCHGIGITNINCSGHIWVEPATIFPKGMNISIYCOAIAIKNCQ 60
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DB 61 PRKLFYKNGIKERFQITRIKKTARLWYKNFLBPHASMYCTACCPKHFQETLLCGKDIS 120
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DB 121 SGYPDPIDPEVTCVITYEYSGNMTCTMAGKLTYYIDTKVYVHVKSLETEEQOYLTSYIN 180
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DB 181 ISTDLSQGGKKYLVWVOAANALGMEESKQLOIHLDDIYIPSAAVISRAETINATVPKTI 240
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DB 301 KRYQPMSSLPFHKTPEVTPVOTSKAFQHDWTNLSGLTVASISTGHLTSDNKGDIQLLGM 360
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DB 361 IVFAVMTLSILSIGIFNSPRTGIRRIILLIPKALYEDIPNMKNSNVVKMLQENSELMN 420
QY 421 NNSBQVLYVDPMTIEIKGIFIPERKPTDYKKNNGSLPETYDPNSLPDNTTVVYITDL 480
DB 421 NNSBQVLYVDPMTIEIKGIFIPERKPTDYKKNNGSLPETYDPNSLPDNTTVVYITDL 480
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DB 481 NTGYKPOISNLPBGSHLSNNNEITSLTKPVPVDSLDSGNPNRLQKHNFAPSVSVNSL 540
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DB 541 SNTIFLGLSLILNQGCCSPDIONSVBEETTMLENDSPETIPEQTLDPDEFVSLGIGI 600
QY 601 VNEELPSINTYFPONILSHRNRIISLLEK 629
DB 601 VNEELPSINTYFPONILSHRNRIISLLEK 629

RESULT 2
OSNPO9_HUMAN PRELIMINARY; PRT; 629 AA.
ID OSNPO9_HUMAN PRELIMINARY; PRT; 629 AA.
AC OSNPO9;
DT 01-OCT-2002 (TREMBLrel. 22, Created)
DT 01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBLrel. 26, Last annotation update)
DE Interleukin-23 receptor
GN Name=IL23R; Synonyms=IL-23R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RX MEDLINE=22018152; PubMed=12023369;
RA Parham C., Chirica M., Timane J., Valisberg E., Travis M., Cheung J.,
RA Pfanz S., Zhang R., Singh K.P., Vega F., To W., Wagner J.,
RA O'Farrell A.-M., McClanahan T., Zurawski S., Hannum C., Gorman D.,
RA Renick D.M., Kastelein R.A., de Waal Malefyt R., Moore K.W.;
RT "A receptor for the heterodimeric cytokine IL-23 is composed of IL-
RT 12beta1 and a novel cytokine receptor subunit, IL-23R."
RL J. Immunol. 168:5699-5708(2002).
DR EMBL; AF461422; AAM44229.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR Ensembl; ENSG00000162594; Homo sapiens.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0004872; F:receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; fn3; 1.
DR SMART; SMO0060; FN3; 1.
DR PROSITE; PS50853; FN3; 2.
DR Receptor.
SQ SEQUENCE 629 AA; 71706 MW; C4228CDA7CGB425 CRC64;

Query Match 99.8%; Score 3327; DB 2; Length 629;
Best Local Similarity 99.8%; Pred. No. 1,66-211;
Matches 628; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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DB 61 PRKLFYKNGIKERFQITRIKKTARLWYKNFLBPHASMYCTACCPKHFQETLLCGKDIS 120
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DB 121 SGYPDPIDPEVTCVITYEYSGNMTCTMAGKLTYYIDTKVYVHVKSLETEEQOYLTSYIN 180
QY 181 ISTDLSQGGKKYLVWVOAANALGMEESKQLOIHLDDIYIPSAAVISRAETINATVPKTI 240
DB 181 ISTDLSQGGKKYLVWVOAANALGMEESKQLOIHLDDIYIPSAAVISRAETINATVPKTI 240
QY 241 YMDSGTTIEKYSCEMRKATNTQTNWYKSPDNTFYVOOSFYLEPNIKYVFORCQDTG 300
DB 241 YMDSGTTIEKYSCEMRKATNTQTNWYKSPDNTFYVOOSFYLEPNIKYVFORCQDTG 300
QY 301 KRYQPMSSLPFHKTPEVTPVOTSKAFQHDWTNLSGLTVASISTGHLTSDNKGDIQLLGM 360
DB 301 KRYQPMSSLPFHKTPEVTPVOTSKAFQHDWTNLSGLTVASISTGHLTSDNKGDIQLLGM 360
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GenCore version 5.1.7
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OM protein - protein search, using SW model

Run on: April 3, 2006, 08:24:45 ; Search time 26.5041 Seconds
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1962.071 Million cell updates/sec

Title: US-10-715-667-21

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Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

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Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 100 summaries

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Pred. No. is the number of results predicted by chance to have a
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and is derived by analysis of the total score distribution.

SUMMARIES

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5	222	6.7	862	1	US-08-915-495-2
6	222	6.7	862	1	US-08-914-520-2
7	222	6.7	862	2	US-09-853-180B-4
8	222	6.7	864	2	US-09-949-016-7758
9	220	6.6	859	2	US-09-313-942-7
10	220	6.6	859	2	US-10-282-162-7
11	217	6.5	918	1	US-08-825-558-6
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13	215	6.4	918	2	US-09-853-180B-3
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23	212	6.4	708	1	US-09-059-099-2
24	212	6.4	708	2	US-09-058-264-2
25	212	6.4	708	2	US-09-455-962-2
26	212	6.4	708	4	PCT-US95-06530-2
27	210	6.3	1158	2	US-09-313-942-26

28	210	6.3	1158	2	US-10-282-162-26	Sequence 26, App1
29	210	6.3	1158	2	US-09-313-942-24	Sequence 24, App1
30	210	6.3	1168	2	US-10-282-162-24	Sequence 24, App1
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43	194	5.8	1097	1	US-08-347-003-6	Sequence 6, App1
44	194	5.8	1097	1	US-09-949-016-6209	Sequence 6209, Ap
45	194	5.8	1119	2	US-09-949-016-10081	Sequence 10081, A
46	191	5.7	599	2	US-09-000-145-2	Sequence 2, App1
47	191	5.7	637	2	US-09-949-016-10128	Sequence 10128, A
48	186.5	5.6	837	1	US-07-923-976-2	Sequence 2, App1
49	180	5.4	620	1	US-08-419-652-7	Sequence 7, App1
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51	176.5	5.3	719	1	US-08-347-003-4	Sequence 4, App1
52	170	5.1	771	1	US-07-923-976-6	Sequence 6, App1
53	170	5.1	783	6	542248-2	Patent No. 542248
54	170	5.1	836	1	US-07-923-976-4	Sequence 4, App1
55	170	5.1	863	1	US-07-923-976-8	Sequence 8, App1
56	167	5.0	572	1	US-08-419-652-5	Sequence 5, App1
57	164.5	4.9	385	2	US-09-071-224-19	Sequence 19, App1
58	164.5	4.9	405	2	US-09-012-072-2	Sequence 2, App1
59	164.5	4.9	405	2	US-09-120-601-2	Sequence 2, App1
60	164.5	4.9	425	2	US-09-071-224-6	Sequence 6, App1
61	163.5	4.9	303	2	US-09-071-224-21	Sequence 21, App1
62	163.5	4.9	389	2	US-09-071-224-24	Sequence 24, App1
63	163.5	4.9	389	2	US-09-071-224-27	Sequence 27, App1
64	163.5	4.9	389	2	US-09-071-224-29	Sequence 29, App1
65	163.5	4.9	422	2	US-09-071-224-12	Sequence 12, App1
66	162.5	4.9	303	2	US-09-071-224-23	Sequence 23, App1
67	162.5	4.9	385	2	US-09-071-224-20	Sequence 20, App1
68	162.5	4.9	388	2	US-09-071-224-17	Sequence 17, App1
69	162.5	4.9	389	2	US-09-071-224-22	Sequence 22, App1
70	162.5	4.9	389	2	US-09-071-224-26	Sequence 26, App1
71	162.5	4.9	392	2	US-09-071-224-18	Sequence 18, App1
72	162.5	4.9	410	2	US-09-521-335-12	Sequence 12, App1
73	162.5	4.9	422	2	US-09-866-028-32	Sequence 32, App1
74	162.5	4.9	422	2	US-09-944-457-32	Sequence 32, App1
75	162.5	4.9	422	2	US-09-945-584-32	Sequence 32, App1
76	162.5	4.9	422	2	US-09-944-944-32	Sequence 32, App1
77	162.5	4.9	422	2	US-09-945-587-32	Sequence 32, App1
78	162.5	4.9	425	2	US-09-071-224-4	Sequence 4, App1
79	162.5	4.9	434	2	US-09-012-072-4	Sequence 4, App1
80	162.5	4.9	434	2	US-09-120-601-4	Sequence 4, App1
81	162.5	4.9	448	2	US-09-120-601-6	Sequence 6, App1
82	161.5	4.8	349	2	US-08-806-597A-14	Sequence 14, App1
83	161.5	4.8	349	2	US-08-970-428A-18	Sequence 18, App1
84	161.5	4.8	389	2	US-09-071-224-28	Sequence 28, App1
85	161.5	4.8	389	2	US-09-071-224-30	Sequence 30, App1
86	160.5	4.8	389	2	US-09-071-224-31	Sequence 31, App1
87	160.5	4.8	407	2	US-09-521-335-13	Sequence 13, App1
88	159.5	4.8	389	2	US-09-071-224-25	Sequence 25, App1
89	157	4.7	592	2	US-09-000-145-6	Sequence 6, App1
90	155	4.6	593	2	US-08-618-957A-11	Sequence 11, App1
91	154	4.6	883	1	US-08-982-430-1	Sequence 1, App1
92	153	4.6	1165	2	US-09-000-145-4	Sequence 4, App1
93	153	4.6	1165	2	US-08-599-455B-4	Sequence 4, App1
94	153	4.6	1165	2	US-09-093-814-1	Sequence 1, App1
95	153	4.6	1165	2	US-09-069-781B-4	Sequence 4, App1
96	153	4.6	1165	2	US-08-618-957A-11	Sequence 11, App1
97	153	4.6	1165	2	US-09-137-132-4	Sequence 4, App1
98	153	4.6	1165	2	US-09-094-410-4	Sequence 4, App1
99	153	4.6	1165	2	US-08-708-123D-4	Sequence 4, App1
100	153	4.6	1165	2	US-08-583-153A-4	Sequence 4, App1

ALIGNMENTS

RESULT 1
US-09-853-180B-2

Sequence 2, Application US/09853180B

Patent No. 6756481

GENERAL INFORMATION:

APPLICANT: Chirica, Madaline

APPLICANT: Parham, Christi L.

APPLICANT: Kastelein, Robert A.

APPLICANT: Moore, Kevin W.

TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.

FILE REFERENCE: DKO1074

CURRENT APPLICATION NUMBER: US/09/853,180B

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 60/203,426

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: PatentIn version 3.2

SEQ ID NO 2

LENGTH: 629

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (-21)..(-21)

OTHER INFORMATION: The 'Xaa' at location -21 stands for Gln, or His.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (126)..(126)

OTHER INFORMATION: The 'Xaa' at location 126 stands for Gly, or Arg.

US-09-853-180B-2

Query Match

Best Local Similarity 99.4%; Score 3314; DB 2; Length 629;

Matches 626; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

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QY 1 MNQVITQMDAVIALYILFSMCHGIGITNINSGHIVWEPAITFRKMGNISYCOAIIKNCQ 60
DB 1 MNQVITQMDAVIALYILFSMCHGIGITNINSGHIVWEPAITFRKMGNISYCOAIIKNCQ 60
QY 61 PRKHFYNGIKERFOITRINKTARLWYKFLPHASMYCTACPCPKFOETLIGKDIS 120
DB 61 PRKHFYNGIKERFOITRINKTARLWYKFLPHASMYCTACPCPKFOETLIGKDIS 120
QY 61 PRKHFYNGIKERFOITRINKTARLWYKFLPHASMYCTACPCPKFOETLIGKDIS 120
DB 61 PRKHFYNGIKERFOITRINKTARLWYKFLPHASMYCTACPCPKFOETLIGKDIS 120
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DB 121 SGYPPIDEVTQVYEVSGNMCTWNAKGLTYIDTKYVHVKSLETEBOQYLTSYIN 180
QY 121 SGYPPIDEVTQVYEVSGNMCTWNAKGLTYIDTKYVHVKSLETEBOQYLTSYIN 180
DB 121 SGYPPIDEVTQVYEVSGNMCTWNAKGLTYIDTKYVHVKSLETEBOQYLTSYIN 180
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DB 181 ISTDSLQGGKYLWVQAANALGMEESKQLQIHLDIVIPSAVISAETINATVPKTI 240
QY 181 ISTDSLQGGKYLWVQAANALGMEESKQLQIHLDIVIPSAVISAETINATVPKTI 240
DB 181 ISTDSLQGGKYLWVQAANALGMEESKQLQIHLDIVIPSAVISAETINATVPKTI 240
QY 241 YWDSQTTIEKUSCEMRKYATNTQWNVGFPDNTFYVOSEFYLEBNIKYVQVRCQEG 300
DB 241 YWDSQTTIEKUSCEMRKYATNTQWNVGFPDNTFYVOSEFYLEBNIKYVQVRCQEG 300
QY 241 YWDSQTTIEKUSCEMRKYATNTQWNVGFPDNTFYVOSEFYLEBNIKYVQVRCQEG 300
DB 241 YWDSQTTIEKUSCEMRKYATNTQWNVGFPDNTFYVOSEFYLEBNIKYVQVRCQEG 300
QY 301 KRYWQMSLFFHKPTEVPOVTSKAFQHDYVNSGLTVASISTGHLTSDNRDGLLGM 360
DB 301 KRYWQMSLFFHKPTEVPOVTSKAFQHDYVNSGLTVASISTGHLTSDNRDGLLGM 360
QY 301 KRYWQMSLFFHKPTEVPOVTSKAFQHDYVNSGLTVASISTGHLTSDNRDGLLGM 360
DB 301 KRYWQMSLFFHKPTEVPOVTSKAFQHDYVNSGLTVASISTGHLTSDNRDGLLGM 360
QY 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYDIIPMKNSNVVKMLQENSELMAN 420
DB 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYDIIPMKNSNVVKMLQENSELMAN 420
QY 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYDIIPMKNSNVVKMLQENSELMAN 420
DB 361 IYFAVWLSTLSLIGIFNRSFRGTGIRKRIILLIPKMLYDIIPMKNSNVVKMLQENSELMAN 420
QY 421 NNSSEVLYVDPMTIEKIFIPBKPTDYKKNCGPLRTROYRONSLEPNTTVPYIPDL 480
DB 421 NNSSEVLYVDPMTIEKIFIPBKPTDYKKNCGPLRTROYRONSLEPNTTVPYIPDL 480
QY 421 NNSSEVLYVDPMTIEKIFIPBKPTDYKKNCGPLRTROYRONSLEPNTTVPYIPDL 480
DB 421 NNSSEVLYVDPMTIEKIFIPBKPTDYKKNCGPLRTROYRONSLEPNTTVPYIPDL 480
QY 481 NNGYKQIINFLPEGSHLNNNEITSLTKPVDYSLDSGNPRLQGHIPAFSVSVNSL 540
DB 481 NNGYKQIINFLPEGSHLNNNEITSLTKPVDYSLDSGNPRLQGHIPAFSVSVNSL 540
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DB 481 NNGYKQIINFLPEGSHLNNNEITSLTKPVDYSLDSGNPRLQGHIPAFSVSVNSL 540
QY 541 SNTIFLGEBSLIINQGCSSPDIONSVEESTTMLLENDSPSETIPROTLTPDEVSCLGI 600
DB 541 SNTIFLGEBSLIINQGCSSPDIONSVEESTTMLLENDSPSETIPROTLTPDEVSCLGI 600
QY 601 VNEELPSINTYFPONILSHFNRIISLEK 629
DB 601 VNEELPSINTYFPONILSHFNRIISLEK 629
```

RESULT 2

US-09-313-942-9

Sequence 9, Application US/09313942

Patent No. 6472179

GENERAL INFORMATION:

APPLICANT: REGENERON PHARMACEUTICALS, INC.

TITLE OF INVENTION: RECEPTOR BASED ANTAGONISTS, AND METHODS OF MAKING

TITLE OF INVENTION: AND USING

FILE REFERENCE: RSG 203-A

CURRENT APPLICATION NUMBER: US/09/313,942

CURRENT FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 09/313,942

PRIOR FILING DATE: 1999-05-19

PRIOR APPLICATION NUMBER: 60/101,858

PRIOR FILING DATE: 1998-09-25

NUMBER OF SEQ ID NOS: 32

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 9

LENGTH: 951

TYPE: PRT

ORGANISM: Homo sapiens

US-09-313-942-9

Query Match

Best Local Similarity 7.0%; Score 232; DB 2; Length 951;

Matches 165; Conservative 122; Mismatches 276; Indels 234; Gaps 41;

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QY 4 VTIQMDAVIALYILFSMCHGIGITNINSGHIVWEPAITFRKMGNISYCOAIIKNCQ 63
DB 2 VTIQMDAVIALYILFSMCHGIGITNINSGHIVWEPAITFRKMGNISYCOAIIKNCQ 63
QY 64 LHFYNGI-----KERFOITRINKTARLWYKFLPHASMYCTACPCPKFOETL 113
DB 58 FHNANAYIVMKTNFTPKQYTI--INRTASSYTFDIASLNTQTLNLTLPQLEBN-- 114
QY 114 ICGDISGYPPIDEVTQVYEVSGNMCTWNAKGLTYIDTKYVHVKSLETEBOQYLTSYIN 161
DB 115 VYGITISGLPBPKNKLSCLVNE--GKMGRCMDGREGTHLETNFTLSKSWATHKFADCK 173
QY 162 -VKSLETEBOQYLTSYINISTDSLQGGKYLWVQAANALGMEESKQLQIHLDIV-- 218
DB 174 AKRDPISCTVDYSGYVYVNI-----VWVEKMLGKVTSD--HINFPVYKV 220
QY 219 ---IPSAVISRAETINATVPKTIYVDSQ--TIEKUSCEMRKYATNTQWNV--VKEPDT 272
DB 221 KENPHNISVINSELSILKLT--WTNPSIKSYILIKNIQRTKQASTMSQIPREDT 277
QY 273 NETYVQOSEFYLEBNIKYVPOVRC--QETGKRYWQMS-----SLFFHKT 315
DB 278 ASTRSSFTVQDLKPTBYVFRIRCKMDQKQWMSSEASQIYEDRPSKAPSPWYKID 337
QY 316 P-----ETVP--QVTSKAFQHDY--WNSGL--TV--ASISTGHLTSDNRG 352
DB 338 PSHTQGYRVLQVWMTLPPFPAANGKILDYEVTLTRWKSHLQNYTVNATGLTVNLINDR-- 395
QY 353 DIGLLGMIVFAVWLSTLSLIGIFN-----RSF----- 380
DB 356 -----YATTLTVKMLVGSKDAAVLITPACFOATHPMDLKAFFKDMMLVWETWT 445
QY 381 -RTGIRKRIILLIPKMLYDIIPMKNSNVVKMLQENSEL-----MNNNSSEVLY--VDP 432
DB 381 -RTGIRKRIILLIPKMLYDIIPMKNSNVVKMLQENSEL-----MNNNSSEVLY--VDP 432
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:22:41 ; Search time 60.2709 Seconds

(without alignments)
2595.264 Million cell updates/sec

Title: US-10-715-667-25

Perfect score: 1934

Sequence: 1 MNQVITQMAVIALYILFSW.....TVASISTGHTLSGLKGSYC 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2443163 seqs, 439378781 residues

Total number of hits satisfying chosen parameters: 2443163

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database :

1: Geneseqp21008:*

2: Geneseqp19908:*

3: Geneseqp20008:*

4: Geneseqp20018:*

5: Geneseqp20028:*

6: Geneseqp20038:*

7: Geneseqp20048:*

8: Geneseqp20058:*

9: Geneseqp20068:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1934	100.0	356	5	Aae24035 Human hae
2	1888	97.6	428	4	Aab74966 Human hae
3	1888	97.6	629	4	Aab74967 Human hae
4	1888	97.6	629	5	Aae24033 Human hae
5	1881	97.3	384	4	Aab86646 Human hae
6	1881	97.3	384	5	Aae24036 Human hae
7	1881	97.3	384	7	Adc07117 Human DNA
8	1881	97.3	384	9	Adc265012 DNAX cyto
9	1871	96.7	428	4	Aab74964 Human hae
10	1871	96.7	629	4	Aab74965 Human hae
11	1868	96.6	629	8	Aad14008 Human DNA
12	1868	96.6	629	8	Ad873605 Human IL-
13	1868	96.6	629	9	Aeas1090 Human DNA
14	1732	89.6	565	5	Aae24034 Human hae
15	1732	89.6	337	4	Aab74963 Human hae
16	1417.5	73.3	644	5	Aae24038 Mouse hae
17	1020.5	52.8	344	5	Aae24030 Mouse hpr
18	261.5	13.5	917	2	Aar26334 gp130. 2/
19	261.5	13.5	917	3	Aay55073 Mouse gp1
20	261.5	13.5	917	8	Adt66596 Murine in
21	230.5	11.9	918	7	Ades8225 Rat Prote
22	230.5	11.9	918	8	Adt66594 Rat inter
23	227	11.7	861	5	Abb78098 Amino aci
24	227	11.7	861	5	Abb78097 Amino aci

25	222	11.5	862	2	AAW12771 Human int
26	222	11.5	862	7	AdB39704 Human int
27	222	11.5	862	7	AdF76395 Novel hum
28	222	11.5	862	8	AdK90609 Human IL-
29	222	11.5	862	8	AdM33832 Human IL-
30	222	11.5	862	8	AdO19580 Human PRO
31	222	11.5	862	8	AdP54649 Human PRO
32	222	11.5	862	9	AdY19580 PRO polyp
33	222	11.5	862	9	AdY15768 PRO polyp
34	222	11.5	862	9	Aeas1092 Human IL-
35	215.5	11.1	727	3	AAW92192 Human gp1
36	215.5	11.1	738	3	AAW92194 Human gp1
37	215.5	11.1	859	2	AAW70796 Human gp1
38	215.5	11.1	859	3	AAW92184 Human gp1
39	215.5	11.1	859	3	ABW02164 Human gp1
40	215.5	11.1	951	2	AAW70798 Human gp1
41	215.5	11.1	951	7	AAW92186 Human gp1
42	215.5	11.1	951	7	ABW02166 Human gp1
43	215.5	11.1	961	3	AAW92187 Human gp1
44	213	11.0	332	2	AAW70799 Human gp1
45	213	11.0	332	3	AAW92188 Human gp1
46	213	11.0	332	7	ABW02167 Human gp1
47	212.5	11.0	658	2	AAW94576 Human gp1
48	212.5	11.0	918	2	AAW10545 Human gp1
49	212.5	11.0	918	2	AAW46233 Human sol
50	212.5	11.0	918	2	AAW75368 Human gp1
51	212.5	11.0	918	3	AAW44694 Human gp1
52	212.5	11.0	918	5	ABJ05551 Breast ca
53	212.5	11.0	918	6	ABR47497 Breast ca
54	212.5	11.0	918	7	ADP17837 Human PRO
55	212.5	11.0	918	7	ADP17837 Human PRO
56	212.5	11.0	918	7	ADN38756 Cancer/ant
57	212.5	11.0	918	8	ADT66592 Human int
58	212.5	11.0	918	8	Aeas1091 Human IL-
59	211.5	10.9	708	2	AAW85911 gp130 N-t
60	211.5	10.9	918	9	ADY15430 PRO polyp
61	211.5	10.9	918	9	ADY16528 PRO polyp
62	211.5	10.9	918	9	ADY16723 PRO polyp
63	208	10.8	326	9	ADW12649 Human gp1
64	208	10.8	329	8	AAW17859 Rheumatol
65	208	10.8	329	8	ADRI4425 Human NF-
66	207.5	10.7	488	5	AAE23860 Human Ob
67	207.5	10.7	488	5	ADG62980 Human gp1
68	207.5	10.7	488	5	ADU75498 Human int
69	207.5	10.7	809	5	AAW92205 Fusion po
70	207.5	10.7	1158	7	ABW02178 Human cyt
71	207.5	10.7	1158	3	AAW92204 Fusion po
72	207.5	10.7	1158	7	ABW02177 Human cyt
73	207.5	10.7	329	9	ADY15432 PRO polyp
74	207	10.7	708	2	AAW37804 Human gp1
75	199.5	10.3	36	4	ABW3440 Peptide #
76	196	10.1	837	8	ADG59673 Murine GC
77	186.5	9.6	837	8	AEB10863 Mouse G-C
78	186.5	9.6	837	2	AAW14254 Murine GC
79	182.5	9.4	837	2	AAW37806 Human LIF
80	182	9.4	1001	2	AAW9508 Human LIF
81	182	9.4	1097	2	AAW45776 Human LIF
82	182	9.4	1097	2	AAW4097 Human LIF
83	182	9.4	1097	8	ABW84695 Human can
84	182	9.4	1119	4	ABW12320 Human LIF
85	182	9.4	1119	4	ABW10125 LIF-R-GBP
86	182	9.4	1522	2	AAW91125 LIF-R-GBP
87	181	9.4	1001	2	AAW99140 Ligand bl
88	180	9.3	334	2	AAW4095 Human LIF
89	177.5	9.2	1001	2	AAW25068 hLIF-R. 3
90	177	9.2	1001	2	AAW9506 Human LIF
91	174	9.0	1001	2	AAW86868 IgG1 Fc r
92	172.5	8.9	984	2	AAW14256 Human GCS
93	170	8.8	771	2	AAW11741 Granulocy
94	170	8.8	783	2	AAW77868 Human pla
95	170	8.8	783	2	AAW10485 Human gra
96	170	8.8	800	2	AAW10486 Human gra
97	170	8.8	800	2	AAW10486 Human gra

98 170 8.8 801 2 AAR11742
99 170 8.8 814 4 AAR30069
100 170 8.8 824 4 AAR23678

AAR11742 Clone 25-
AAR30069 Novel hum
AAR23678 Human BST

ALIGNMENTS

RESULT 1

AAE24035 AAE24035 standard; protein; 356 AA.

AC AAE24035;

DT 23-SEP-2002 (first entry)

DE Human haematopoietin receptor_2 (HPR2) ex9 protein.

Human haematopoietin receptor; receptor; HPR1; HPR2; cell proliferation;
pancytopenia; leukopenia; anaemia; thrombocytopenia; osteoporosis;
neurodegenerative disorder; leukaemia; carcinoma; haematologic disorder;
cancer; myelodysplastic syndrome; idiopathic thrombocytopenic purpura;
ITP; sickle cell vasocclusive crisis; myelofibrosis; myeloid metaplasia;
osteoclast disorder; periodontitis; acute polyneuropathy; Bell's palsy;
anorexia nervosa; chronic fatigue syndrome; Creutzfeld-Jacob disease;
demyelinating neuropathy; Guillain-Barre syndrome; Gulf war syndrome;
vertebral disc disease; myasthenia gravis; chronic neuronal degeneration;
stroke; fatigue; tumour; sarcoma; osteoporosis; obesity; infertility;
ischaemic disease.

OS Homo sapiens.

FN WO200229060-A2.

PD 11-APR-2002.

PF 05-OCT-2001; 2001WO-US031634.

PR 06-OCT-2000; 2000US-0238706P.

PR 13-OCT-2000; 2000US-0240476P.

PR 20-FEB-2001; 2001US-0270282P.

PA (IMMV) IMMUNEX CORP.

PI Coeman DJ, Mosley BA, Bird TA, Dubose RF, Wiley SR,

DR WPI; 2002-330172/36.

DR N-PsDB; AAD38775.

PT Human and murine haematopoietin receptor polypeptides HPR1 and HPR2,
PT useful for treating cell proliferation, metabolic, and reproductive
PT hormone related conditions.

PS Claim 3; Page 127-129; 136p; English.

XX The present invention relates to human and murine haematopoietin receptor
XX polypeptides HPR1 and HPR2. Sequences of the invention are useful for
XX treating cell proliferation conditions e.g., pancytopenia, leukopenia,
XX anaemia, thrombocytopenia, neurodegenerative disorders and osteoporosis
XX resulting from a lack of bone-forming cells. They are also useful for
XX treating cell proliferation conditions such as leukaemia and tumour
XX metastasis, osteoporosis resulting from an excess of bone-resorbing
XX cells. HPR sequences are also useful for treating medical conditions and
XX diseases such as cell proliferation, metabolic and reproductive hormone
XX related conditions. They are useful for treating various haematologic and
XX oncologic disorders e.g., Epstein-Barr virus-positive nasopharyngeal
XX carcinoma, myelogenous leukemia, colon, stomach, prostate, renal cell,
XX cervical and ovarian cancers, lung cancer (SCLC and NSCLC), including
XX cancer-associated cachexia, fatigue, solid tumours (e.g., osteosarcoma,
XX sarcoma), carcinoma (e.g., adenocarcinoma (for example, breast cancer),
XX squamous cell carcinoma), haematologic disorders, anaemias (e.g., anaemia
XX of chronic disease, aplastic anaemia, Fanconi's aplastic anaemia), myelo-
XX dysplastic syndromes (including refractory anaemia, refractory anaemia

CC with ringed sideroblasts or with excess blasts), idiopathic thrombocyto-
CC paenic purpura (ITP), sickle cell vasocclusive crisis, myelofibrosis/
CC myeloid metaplasia, osteoclast disorders that lead to bone loss such as
CC osteoporosis including post-menopausal osteoporosis, periodontitis
CC resulting in tooth loosening or loss, prosthesis loosening after joint
CC replacement, neurodegenerative conditions (e.g., acute polyneuropathy,
CC Bell's palsy, anorexia nervosa, chronic fatigue syndrome, transmissible
CC dementia including Creutzfeld-Jacob disease, demyelinating neuropathy,
CC Guillain-Barre syndrome, vertebral disc disease, Gulf war syndrome,
CC myasthenia gravis, chronic neuronal degeneration, stroke including
CC cerebral ischaemic diseases. HPR1 and HPR2 polypeptides are also useful
CC for treating various other disorders such as osteoporosis, obesity,
CC deficient mammary development and infertility. The present sequence is
CC human HPR2 ex9 protein

CC Sequence 356 AA;

Query Match 100.0%; Score 1934; DB 5; Length 356;

Best Local Similarity 100.0%; Pred. No. 4,1e-162;

Matches 356; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MNQVTTQMDAVIALYLLFSMCHGGITTNINCSGHVWEPAITFKMGAMNISIYQAAIRKQ 60
QY 61 PRKLFYKNGIKERQITRIKKTARLWYKQFLBPHASMYCTAECQKHPQETLLIGKDIS 120
DB 61 PRKLFYKNGIKERQITRIKKTARLWYKQFLBPHASMYCTAECQKHPQETLLIGKDIS 120
QY 121 SGYPDPIDPEVTCVYIEYSGNMTCTMNAKLTLYIDTKYVHVKSLETSBEOQYLTSSYIN 180
DB 121 SGYPDPIDPEVTCVYIEYSGNMTCTMNAKLTLYIDTKYVHVKSLETSBEOQYLTSSYIN 180
QY 181 ISTDSLQGGKTYLVWVQAAALQMESKQLOIHLDDIYIPSAVYSRAETINATYPKTII 240
DB 181 ISTDSLQGGKTYLVWVQAAALQMESKQLOIHLDDIYIPSAVYSRAETINATYPKTII 240
QY 241 YWDSOTTEKXSCERRYKATNTQTNVKEPDTNFTYVOOSELYLPNIRKYVQVCOENG 300
DB 241 YWDSOTTEKXSCERRYKATNTQTNVKEPDTNFTYVOOSELYLPNIRKYVQVCOENG 300
QY 301 KRYWQMSLSFPHKTPETVPQVTSKAFQHDITWNSGLTVASISTGHLTSGLKSGSYC 356
DB 301 KRYWQMSLSFPHKTPETVPQVTSKAFQHDITWNSGLTVASISTGHLTSGLKSGSYC 356

RESULT 2

AAE24035 AAE24035 standard; protein; 428 AA.

AC AAE24035;

DT 11-JUL-2001 (first entry)

DE Human haematopoietin receptor protein NR12.4 SEQ ID NO:8.

XX Human; haematopoietin receptor protein; NR12; immunosuppressive;
XX antiallergic; haematopoietin factor; autoimmune disease; tissue rejection;
XX metal allergy; pollen allergy.

OS Homo sapiens.

FN WO200123556-A1.

PD 05-APR-2001.

PF 27-SEP-2000; 2000WO-JP006654.

PR 27-SEP-1999; 99JP-00273358.

PR 03-AUG-2000; 2000JP-00240397.

PA (CHUGAI) CHUGAI RES INST MOLECULAR MEDICINE INC.

GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:22:56 ; Search time 99.9157 Seconds
(without alignments)
2513.799 Million cell updates/sec

Title: US-10-715-667-25

Sequence: 1 MNOVTIQMDAYALATILPSM.....TVASISTGHLTSGLRKSGSYC 356

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 2166443 segs, 705528306 residues

Total number of hits satisfying chosen parameters: 2166443

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 100 summaries

Database : uniprot_05.80:*
1: uniprot_sprot:*
2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1888	97.6	629	05VWK5_HUMAN	05VWK5 homo sapien
2	1881	97.3	629	08NFO9_HUMAN	08NFO9 homo sapien
3	1720	88.9	320	04VGP1_HUMAN	04VGP1 homo sapien
4	1701	88.0	320	04VGP3_HUMAN	04VGP3 homo sapien
5	1674	86.6	593	04VGP6_HUMAN	04VGP6 homo sapien
6	1421.5	73.5	644	08K4B4_MOUSE	08K4B4 mus musculu
7	705	36.5	138	04VGP5_HUMAN	04VGP5 homo sapien
8	511	26.4	375	04VGP4_HUMAN	04VGP4 homo sapien
9	449	23.2	390	05VWK7_HUMAN	05VWK7 homo sapien
10	442	22.9	391	09GAS1_HUMAN	09GAS1 homo sapien
11	329.5	17.0	869	05GR16_CHICK	05GR16 gallus gall
12	281.5	14.6	918	09W6U9_CHICK	09W6U9 gallus gall
13	277	14.3	554	06UAM2_TETNG	06UAM2 tetraodon n
14	261.5	13.5	917	1L6RB_MOUSE	1L6RB mus musculu
15	261.5	13.5	917	06PD19_MOUSE	06PD19 mus musculu
16	253.5	13.0	874	112R2_MOUSE	112R2 mus musculu
17	252	13.0	861	112R2_BOVIN	09B6G2 bos taurus
18	246.5	12.7	881	057515_XENLA	057515 xenopus lae
19	245.5	12.7	1010	07T089_RAT	07T089 rattus norv
20	240.5	12.4	813	06UAM1_TETNG	06UAM1 tetraodon n
21	230.5	11.9	858	1L6RB_RAT	1L6RB rattus norv
22	230	11.9	858	04QYCB_CANPA	04QYCB canis fami
23	223	11.5	861	112R2_PIG	08NFS1 sus scrofa
24	222	11.5	862	112R2_HUMAN	09G6E5 homo sapien
25	222	11.5	862	05VWK8_HUMAN	05VWK8 homo sapien
26	212.5	11.0	918	1L6RB_HUMAN	1L6RB homo sapien
27	211.5	10.9	857	05FC04_HUMAN	05FC04 homo sapien
28	211	10.9	2030	04S3E8_TETNG	04S3E8 tetraodon n
29	197.5	10.2	813	06DD37_XENLA	06DD37 xenopus lae
30	189	9.8	394	06UAM5_TETNG	06UAM5 tetraodon n
31	187	9.7	1097	05XMR9_CANPA	05XMR9 canis fami

32	186.5	9.6	837	1	CSFR_MOUSE	P40223 mus musculu
33	186	9.6	477	2	05F3Y5_CHICK	05F3Y5 gallus gall
34	182	9.4	1097	1	1LFR_HUMAN	P42702 homo sapien
35	178.5	9.2	739	2	04T141_TETNG	04T141 tetraodon n
36	178.5	9.2	870	2	06UAM0_TETNG	06UAM0 tetraodon n
37	175	9.0	617	2	07SS21_RANCA	07SS21 rana catesb
38	172	8.9	389	2	06D328_BRARE	06D328 brachydano
39	170	8.8	836	1	CSFR3_HUMAN	099662 homo sapien
40	168	8.7	719	2	0510Y2_MOUSE	0510Y2 mus musculu
41	168	8.7	1092	1	1LFR_MOUSE	P42703 mus musculu
42	167	8.6	425	1	CRLE1_HUMAN	09JMB8 mus musculu
43	162.5	8.4	422	1	CRLE1_HUMAN	075462 homo sapien
44	161.5	8.4	582	2	06UML6_HUMAN	06UML6 homo sapien
45	161.5	8.4	764	2	06BRC4_HUMAN	06BRC4 homo sapien
46	161	8.3	1093	2	070535_RAT	070535 rattus norv
47	158	8.2	324	2	06BRC5_HUMAN	06BRC5 homo sapien
48	158	8.2	509	2	08WYJ0_HUMAN	08WYJ0 homo sapien
49	158	8.2	649	2	06BRC6_HUMAN	06BRC6 homo sapien
50	158	8.2	662	2	06BRC3_HUMAN	06BRC3 homo sapien
51	158	8.2	732	2	08N117_HUMAN	08N117 homo sapien
52	158	8.2	819	2	0616F7_EUBMA	0616F7 eublepharis
53	153	7.9	229	2	05VWK6_HUMAN	05VWK6 homo sapien
54	151.5	7.8	547	2	06BAL6_MOUSE	06BAL6 mus musculu
55	151.5	7.8	662	2	06BAL7_MOUSE	06BAL7 mus musculu
56	151.5	7.8	716	2	08K5B1_MOUSE	08K5B1 mus musculu
57	151.5	7.8	716	2	08R501_MOUSE	08R501 mus musculu
58	151.5	7.8	1148	2	091BA7_CHICK	091BA7 gallus gall
59	150.5	7.8	334	2	06U085_CHICK	06U085 gallus gall
60	150.5	7.8	492	2	06NZFO_MOUSE	06NZFO mus musculu
61	150.5	7.8	1148	2	0918V6_CHICK	0918V6 gallus gall
62	150	7.8	622	2	08E5V4_CEBAP	08E5V4 cebus aell
63	147	7.6	288	2	096P36_HUMAN	096P36 homo sapien
64	147	7.6	349	2	090HJ5_HUMAN	090HJ5 homo sapien
65	147	7.6	376	2	096P35_HUMAN	096P35 homo sapien
66	147	7.6	581	1	PRLR_BOVIN	028172 bos taurus
67	147	7.6	622	1	PRLR_HUMAN	P16471 homo sapien
68	147	7.6	622	1	OSRAM0_PONPY	05RAW0 pongo pygma
69	146.5	7.6	437	2	04RMP5_TETNG	04RMP5 tetraodon n
70	146.5	7.6	604	2	08Q654_CYPCA	08Q654 cyprinus ca
71	145.5	7.5	1147	2	09DDK1_MELGA	09DDK1 melagris g
72	143	7.4	581	1	PRLR_SHEEP	046561 ovis aries
73	142.5	7.4	602	2	06UAM2_BRARE	06UAM2 brachydano
74	142	7.3	600	2	09PTP0_CARAU	09PTP0 carassius a
75	141.5	7.3	622	2	09N0U7_CALJA	09N0U7 callithrix
76	141.5	7.3	831	1	PRLR_CHICK	09N0J7 gallus gall
77	141.5	7.3	831	2	06ODAO_CHICK	06ODAO gallus gall
78	140.5	7.3	460	2	07T220_CHICK	07T220 gallus gall
79	140	7.2	268	2	08TD78_HUMAN	08TD78 homo sapien
80	139.5	7.2	609	2	051SE1_CYPCA	051SE1 cyprinus ca
81	138.5	7.2	623	1	127RA_MOUSE	070394 mus musculu
82	136	7.0	360	2	06UAP0_TETNG	06UAP0 tetraodon n
83	136	7.0	818	2	0640Q2_MOUSE	0640Q2 mus musculu
84	136	7.0	1165	1	LEBR_PIG	P48571 sus scrofa
85	136	7.0	1165	1	LEBR_PIG	04W810 canis fami
86	136	7.0	1166	2	04W810_CANPA	04W810 homo sapien
87	133	6.9	659	2	094G138_HUMAN	094G138 homo sapien
88	132.5	6.9	346	2	093404_OREMO	093404 oreochromis
89	132	6.8	881	2	064222_MYOLU	064222 myotis luci
90	132	6.8	1153	2	05XXB8_MYOLU	05XXB8 myotis luci
91	131.5	6.8	831	1	PRLR_MELGA	091094 melagris g
92	131	6.8	1165	1	LEBR_HUMAN	P48357 homo sapien
93	130	6.7	283	3	06UCB4_CHICK	06UCB4 gallus gall
94	130	6.7	581	1	PRLR_CEREL	028353 cervus elap
95	130	6.7	1162	1	LEBR_RAT	062895 rattus norv
96	129.5	6.7	894	2	06UAM7_TETNG	06UAM7 tetraodon n
97	127.5	6.6	227	2	09GLM3_TESMA	09GLM3 ursus marit
98	126.5	6.5	830	1	PRLR_COLLI	090374 columba liv
99	126.5	6.5	1083	2	08QF07_CHICK	08QF07 gallus gall
100	125.5	6.5	310	2	05BDB27_RAT	05BDB27 rattus norv

ALIGNMENTS

```
RESULT 1
OSVWKS_HUMAN
ID OSVWKS_HUMAN PRELIMINARY; PRT; 629 AA.
AC OSVWKS;
DT 01-FEB-2005 (TREMBlrel. 29, Created)
DT 01-FEB-2005 (TREMBlrel. 29, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Interleukin 23 receptor.
GN Name=IL23R; ORFNames=Rpl1-131015.1-001;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Hall R.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
RP NUCLEOTIDE SEQUENCE.
RA Davidson C.;
RL Submitted (MAY-2005) to the EMBL/GenBank/DBJ databases.
DR EMBL; AL389925; CAH70406.1; -; Genomic DNA.
DR EMBL; AL109843; CA12678.1; -; Genomic DNA.
DR EMBL; AL109843; CAH70406.1; JOINED; Genomic DNA.
DR EMBL; AL389925; CA12678.1; JOINED; Genomic DNA.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0016021; C:integral to membrane, IEA.
DR GO; GO:0004872; F:receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; Fn3; 1.
DR PROSITE; PS50853; FN3; 2.
KW Receptor; Repeat; Transmembrane.
SQ SEQUENCE 629 AA; 71722 MW; AC63C89B81AABF05 CRC64;

Query Match 97.6%; Score 1888; DB 2; Length 629;
Best Local Similarity 100.0%; Pred. No. 7,4e-141;
Matches 348; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIMVEPATIFPKGMNISIYCOAIIKNCQ 60
DB 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIMVEPATIFPKGMNISIYCOAIIKNCQ 60
QY 61 PRKLHFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLTCGKD1S 120
DB 61 PRKLHFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLTCGKD1S 120
QY 121 SGYPDPIDDEYTCVLYEYSGNMTCTWNAKGLTYIDTKVHVHVKSLTEEBQOYLTSYIN 180
DB 121 SGYPDPIDDEYTCVLYEYSGNMTCTWNAKGLTYIDTKVHVHVKSLTEEBQOYLTSYIN 180
QY 121 SGYPDPIDDEYTCVLYEYSGNMTCTWNAKGLTYIDTKVHVHVKSLTEEBQOYLTSYIN 180
DB 121 SGYPDPIDDEYTCVLYEYSGNMTCTWNAKGLTYIDTKVHVHVKSLTEEBQOYLTSYIN 180
QY 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
DB 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
QY 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
DB 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
QY 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
DB 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
QY 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
DB 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
QY 301 KRYMQPMSLFFHKTPETVPQVTSKAFQHDWTNSSLTVASISTGHLTS 348
DB 301 KRYMQPMSLFFHKTPETVPQVTSKAFQHDWTNSSLTVASISTGHLTS 348

RESULT 2
OSNFP09_HUMAN
ID OSNFP09_HUMAN PRELIMINARY; PRT; 629 AA.
AC OSNFP09;
DT 01-OCT-2002 (TREMBlrel. 22, Created)
DT 01-OCT-2002 (TREMBlrel. 22, Last sequence update)
DT 01-MAR-2004 (TREMBlrel. 26, Last annotation update)
DE Interleukin-23 receptor.
```

```
GN Name=IL23R; Synonyms=IL-23R;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Parham S., Chirica M., Timans J., Vaisberg E., Travis M., Cheung J.,
RA Pflanz S., Zhang R., Singh K.P., Vega F., To W., Wagner U.,
RA O'Farrell A.-M., McClanahan T., Zurawski S., Hannum C., Gorman D.,
RA Remick D.M., Kastelein R.A., de Waal Malefyt R., Moore K.W.;
RT "A receptor for the heterodimeric cytokine IL-23 is composed of IL-
RT 12beta1 and a novel cytokine receptor subunit, IL-23R."
RL J. Immunol. 168:5699-5708(2002).
DR EMBL; AF461422; AA044229.1; -; mRNA.
DR HSSP; P16471; 1BP3.
DR Ensembl; ENSG00000162594; Homo sapiens.
DR HGNC; HGNC:19100; IL23R.
DR GO; GO:0004872; F:receptor activity, IEA.
DR InterPro; IPR003961; FN_III.
DR Pfam; PF00041; Fn3; 1.
DR SMART; SM00060; FN3; 1.
DR PROSITE; PS50853; FN3; 2.
KW Receptor.
SQ SEQUENCE 629 AA; 71706 MW; C4226CD0A7C6B425 CRC64;

Query Match 97.3%; Score 1881; DB 2; Length 629;
Best Local Similarity 99.7%; Pred. No. 2,7e-140;
Matches 347; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIMVEPATIFPKGMNISIYCOAIIKNCQ 60
DB 1 MNQVTTQMDAVIALYILFSWCHGGITNINCSGHIMVEPATIFPKGMNISIYCOAIIKNCQ 60
QY 61 PRKLHFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLTCGKD1S 120
DB 61 PRKLHFYNGIKERFOITRIKKTARLWYKNFLBPHASMYCTACBPKHFOETLTCGKD1S 120
QY 121 SGYPDPIDDEYTCVLYEYSGNMTCTWNAKGLTYIDTKVHVHVKSLTEEBQOYLTSYIN 180
DB 121 SGYPDPIDDEYTCVLYEYSGNMTCTWNAKGLTYIDTKVHVHVKSLTEEBQOYLTSYIN 180
QY 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
DB 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
QY 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
DB 181 ISTDLSQGGKYLWVVOAANALGMBESKQLOIHLDIVIPSAAVISRATTINATVPKTI 240
QY 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
DB 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
QY 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
DB 241 YMDSQTTIEKYSCEMRKYATTNQTNWVKEPDTNFTYVQOSEFYLEPNIKYVFOVRCQETG 300
QY 301 KRYMQPMSLFFHKTPETVPQVTSKAFQHDWTNSSLTVASISTGHLTS 348
DB 301 KRYMQPMSLFFHKTPETVPQVTSKAFQHDWTNSSLTVASISTGHLTS 348

RESULT 3
Q4VGP1_HUMAN
ID Q4VGP1_HUMAN PRELIMINARY; PRT; 320 AA.
AC Q4VGP1;
DT 13-SEP-2005 (TREMBlrel. 31, Created)
DT 13-SEP-2005 (TREMBlrel. 31, Last sequence update)
DT 13-SEP-2005 (TREMBlrel. 31, Last annotation update)
DE Interleukin 23 receptor isoform 4 (Fragment).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Euarchontoglires; Primates; Catarrhini; Homnidae;
OC Homo.
OC NCBI_TaxID=9606;
RN [1]
RP NUCLEOTIDE SEQUENCE.
RA Zhang X.-Y., Zhang Y., Zhang H.-D., Wang S.-H., Liu L.;
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GenCore version 5.1.7
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OM protein - protein search, using sw model

Run on: April 3, 2006, 08:24:45 ; Search time 15.0008 Seconds
(without alignments)
1962.071 Million cell updates/sec

Title: US-10-715-667-25

Perfect score: 1934

Sequence: 1 MNOVTIQMDAVATLALYILPSW.....TVASISTGHTLSGLKRGSYC 356

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 572060 seqs, 82675679 residues

Total number of hits satisfying chosen parameters: 572060

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 100 summaries

Database : Issued Patents AA:*

- 1: /cgn2_6/prodata/1/1aa/5 COMB. pep:*
- 2: /cgn2_6/prodata/1/1aa/6 COMB. pep:*
- 3: /cgn2_6/prodata/1/1aa/H COMB. pep:*
- 4: /cgn2_6/prodata/1/1aa/PCRTUS COMB. pep:*
- 5: /cgn2_6/prodata/1/1aa/RB COMB. pep:*
- 6: /cgn2_6/prodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1868	96.6	629	2	US-09-853-180B-2
2	222	11.5	862	1	US-08-685-118-2
3	222	11.5	862	1	US-08-915-495-2
4	222	11.5	862	1	US-08-914-520-2
5	222	11.5	862	2	US-09-853-180B-4
6	222	11.5	864	2	US-09-949-016-7758
7	215.5	11.1	859	2	US-09-313-942-7
8	215.5	11.1	859	2	US-10-282-162-7
9	215.5	11.1	951	2	US-09-313-942-9
10	215.5	11.1	951	2	US-10-282-162-9
11	213	11.0	332	2	US-09-313-942-10
12	213	11.0	332	2	US-10-282-162-10
13	212.5	11.0	658	1	US-08-825-558-4
14	212.5	11.0	658	2	US-09-312-611-4
15	212.5	11.0	918	1	US-08-825-558-6
16	212.5	11.0	918	2	US-09-312-611-6
17	212.5	11.0	918	2	US-09-853-180B-3
18	212.5	11.0	918	2	US-09-949-002-333
19	211.5	10.9	708	1	US-07-797-556-2
20	211.5	10.9	708	1	US-08-308-881-2
21	211.5	10.9	708	1	US-09-058-263-2
22	211.5	10.9	708	1	US-09-059-099-2
23	211.5	10.9	708	2	US-09-058-264-2
24	211.5	10.9	708	2	US-09-455-962-2
25	211.5	10.9	708	4	PCR-US95-06530-2
26	211.5	10.9	937	2	US-09-949-002-536
27	207.5	10.7	488	1	US-08-599-455B-5

28	207.5	10.7	488	2	US-09-069-781B-5	Sequence 5, App1
29	207.5	10.7	488	2	US-09-137-132-5	Sequence 5, App1
30	207.5	10.7	488	2	US-08-864-564A-5	Sequence 5, App1
31	207.5	10.7	488	2	US-09-094-410-5	Sequence 5, App1
32	207.5	10.7	488	2	US-08-708-123D-5	Sequence 5, App1
33	207.5	10.7	488	2	US-08-583-153A-5	Sequence 5, App1
34	207.5	10.7	488	2	US-08-638-524B-5	Sequence 5, App1
35	207.5	10.7	1158	2	US-09-313-942-26	Sequence 26, App1
36	207.5	10.7	1158	2	US-10-282-162-26	Sequence 26, App1
37	207.5	10.7	1168	2	US-09-313-942-24	Sequence 24, App1
38	207.5	10.7	1168	2	US-10-282-162-24	Sequence 24, App1
39	186.5	9.6	837	1	US-07-923-976-2	Sequence 2, App1
40	182	9.4	1001	1	US-07-923-976-2	Sequence 2, App1
41	182	9.4	1001	1	US-07-943-843-2	Sequence 2, App1
42	182	9.4	1001	1	US-08-347-003-2	Sequence 2, App1
43	182	9.4	1097	1	US-07-943-843-6	Sequence 6, App1
44	182	9.4	1097	1	US-08-347-003-6	Sequence 6, App1
45	182	9.4	1097	2	US-09-949-016-6209	Sequence 6209, App1
46	182	9.4	1119	2	US-09-949-016-10081	Sequence 10081, App1
47	170	8.8	771	1	US-07-923-976-6	Sequence 6, App1
48	170	8.8	783	6	542248-2	Patent No. 542248
49	170	8.8	836	1	US-07-923-976-4	Sequence 4, App1
50	170	8.8	863	1	US-07-923-976-8	Sequence 8, App1
51	168	8.7	620	1	US-08-419-652-7	Sequence 7, App1
52	168	8.7	719	1	US-07-943-843-4	Sequence 4, App1
53	168	8.7	719	1	US-08-347-003-4	Sequence 4, App1
54	167	8.6	385	2	US-09-071-224-19	Sequence 19, App1
55	167	8.6	405	2	US-09-012-072-2	Sequence 2, App1
56	167	8.6	425	2	US-09-071-224-6	Sequence 6, App1
57	167	8.6	425	2	US-09-071-224-6	Sequence 6, App1
58	166.5	8.6	502	1	US-08-419-652-5	Sequence 5, App1
59	163.5	8.5	373	2	US-09-071-224-21	Sequence 21, App1
60	163.5	8.5	389	2	US-09-071-224-24	Sequence 24, App1
61	163.5	8.5	389	2	US-09-071-224-27	Sequence 27, App1
62	163.5	8.5	389	2	US-09-071-224-29	Sequence 29, App1
63	163.5	8.5	422	2	US-09-071-224-2	Sequence 2, App1
64	163	8.4	407	2	US-09-521-335-13	Sequence 13, App1
65	162.5	8.4	303	2	US-09-071-224-23	Sequence 23, App1
66	162.5	8.4	385	2	US-09-071-224-20	Sequence 20, App1
67	162.5	8.4	388	2	US-09-071-224-17	Sequence 17, App1
68	162.5	8.4	389	2	US-09-071-224-22	Sequence 22, App1
69	162.5	8.4	389	2	US-09-071-224-26	Sequence 26, App1
70	162.5	8.4	392	2	US-09-071-224-18	Sequence 18, App1
71	162.5	8.4	410	2	US-09-521-335-18	Sequence 18, App1
72	162.5	8.4	422	2	US-09-521-335-12	Sequence 12, App1
73	162.5	8.4	422	2	US-09-866-028-32	Sequence 32, App1
74	162.5	8.4	422	2	US-09-944-457-32	Sequence 32, App1
75	162.5	8.4	422	2	US-09-944-944-32	Sequence 32, App1
76	162.5	8.4	422	2	US-09-945-587-32	Sequence 32, App1
77	162.5	8.4	425	2	US-09-071-224-4	Sequence 4, App1
78	162.5	8.4	434	2	US-09-012-072-4	Sequence 4, App1
79	162.5	8.4	434	2	US-09-120-601-4	Sequence 4, App1
80	162.5	8.4	448	2	US-09-120-601-6	Sequence 6, App1
81	161.5	8.4	389	2	US-09-071-224-28	Sequence 28, App1
82	161.5	8.4	389	2	US-09-071-224-30	Sequence 30, App1
83	160.5	8.3	389	2	US-09-071-224-31	Sequence 31, App1
84	159.5	8.2	389	2	US-09-071-224-25	Sequence 25, App1
85	150.5	7.8	349	2	US-08-419-652-6	Sequence 6, App1
86	147	7.6	602	1	US-08-806-597A-14	Sequence 14, App1
87	147	7.6	349	2	US-08-970-428B-14	Sequence 14, App1
88	147	7.6	599	2	US-09-000-145-2	Sequence 2, App1
89	147	7.6	637	2	US-09-949-016-10128	Sequence 10128, App1
90	138.5	7.2	623	1	US-08-653-740-7	Sequence 7, App1
91	138.5	7.2	623	1	US-09-073-954-7	Sequence 7, App1
92	138.5	7.2	623	2	US-09-275-925-7	Sequence 7, App1
93	136	7.0	894	2	US-08-599-455B-2	Sequence 2, App1
94	136	7.0	894	2	US-09-069-781B-12	Sequence 12, App1
95	136	7.0	894	2	US-08-618-957A-12	Sequence 12, App1
96	136	7.0	894	2	US-09-137-132-2	Sequence 2, App1
97	136	7.0	894	2	US-08-864-564A-2	Sequence 2, App1
98	136	7.0	894	2	US-09-094-410-2	Sequence 2, App1
99	136	7.0	894	2	US-08-708-123D-2	Sequence 2, App1
100	136	7.0	894	2	US-08-583-153A-2	Sequence 2, App1

ALIGNMENTS

RESULT 1
US-09-853-180B-2

Sequence 2, Application US/09853180B

Patent No. 6756481

GENERAL INFORMATION:

APPLICANT: Chitica, Madeline

APPLICANT: Parham, Christi L.

APPLICANT: Kastelein, Robert A.

APPLICANT: Moore, Kevin W.

TITLE OF INVENTION: Mammalian Receptor Proteins; Related Reagents and Methods.

FILE REFERENCE: DX01074

CURRENT APPLICATION NUMBER: US/09/853,180B

CURRENT FILING DATE: 2001-05-10

PRIOR APPLICATION NUMBER: 60/203,426

PRIOR FILING DATE: 2000-05-10

NUMBER OF SEQ ID NOS: 4

SOFTWARE: Patentin version 3.2

SEQ ID NO 2

LENGTH: 629

TYPE: PRT

ORGANISM: Homo sapiens

FEATURE:

NAME/KEY: misc_feature

LOCATION: (-21)..(-21)

OTHER INFORMATION: The 'Xaa' at location -21 stands for Gln, or His.

FEATURE:

NAME/KEY: misc_feature

LOCATION: (126)..(126)

OTHER INFORMATION: The 'Xaa' at location 126 stands for Gly, or Arg.

US-09-853-180B-2

Query Match 96.6%; Score 1868; DB 2; Length 629;
Best Local Similarity 99.1%; Pred. No. 2.3e-176;
Matches 345; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

QY 1 MNQVITQMDAVIALYILFSWCHGITNINCSGHIWEPATIFPKMGNISYCOAIRKQ 60
DB 1 MNQVITQMDAVIALYILFSWCHGITNINCSGHIWEPATIFPKMGNISYCOAIRKQ 60
QY 61 PRKHFYNGIKERPOIRINKTARLYKNTLEBHAAMYCTABCPKFOETLIGKDIS 120
DB 61 PRKHFYNGIKERPOIRINKTARLYKNTLEBHAAMYCTABCPKFOETLIGKDIS 120
QY 121 SGYPDIDDEVYCVIYESGNMTCTMNAKLTLYIDTKYVHVKSLETEBEOQYLTSSYN 180
DB 121 SGYPDIDDEVYCVIYESGNMTCTMNAKLTLYIDTKYVHVKSLETEBEOQYLTSSYN 180
QY 181 ISTDSLQGGKYLWVVOAANALGMEESKQIHDIDIVIPSAVISRAETINATVPKTI 240
DB 181 ISTDSLQGGKYLWVVOAANALGMEESKQIHDIDIVIPSAVISRAETINATVPKTI 240
QY 241 YWDSGTTIEKYSCEMRKYATNTQTNVYKFPDNTFTYVVOOSEFYLEPNIKYVQVRCQ 300
DB 241 YWDSGTTIEKYSCEMRKYATNTQTNVYKFPDNTFTYVVOOSEFYLEPNIKYVQVRCQ 300
QY 301 KRYWQPMGSLFFHKTPEYPOVTSKAFQHDWTNSGLTVASISTGHLTS 348
DB 301 KRYWQPMGSLFFHKTPEYPOVTSKAFQHDWTNSGLTVASISTGHLTS 348

RESULT 2

US-08-685-118-2

Sequence 2, Application US/08685118

Patent No. 5840530

GENERAL INFORMATION:

APPLICANT: Gubler, Ulrich A

APPLICANT: Presky, David H

TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRES:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingeland Street

CITY: Nutley

STATE: NJ

COUNTRY: USA

ZIP: 07110

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.30

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/685,118

FILING DATE:

CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:

NAME: Silverman, Robert A.

REGISTRATION NUMBER: 35,682

REFERENCE/DOCKET NUMBER: CD 9195

TELEPHONE: (201) 235-2863

TELEFAX: (201) 235-2363

INFORMATION FOR SEQ ID NO: 2:

SEQUENCE CHARACTERISTICS:

LENGTH: 862 amino acids

TYPE: amino acid

TOPOLOGY: linear

MOLECULE TYPE: protein

US-08-685-118-2

Query Match 11.5%; Score 222; DB 1; Length 862;

Best Local Similarity 24.0%; Pred. No. 8.5e-13;

Matches 76; Conservative 57; Mismatches 130; Indels 54; Gaps 13;

QY 32 GHIWEPATIFPKMGNISYCOAIRKQCPKLFYKNGIKERFOITRINKTARLYK- 90
DB 31 GDVYKPEHVILVLSGVNITC-----SLKPR-----GQCFYSRNKL---ILYK 73
QY 91 ---NFLRPHA-----SMYCTABCPKFOETLIGKDISSGYPDIDDEVY 133
DB 74 DRIIRFHGHSLNSQVTLPLGTLFVCKLAC-INSDEIQCGAEIFGVAPROPONLSC 132
QY 134 VIVESGNMTCTMNAKLTLYIDTKYVHV---KSLTEBEOQYLTSSY----INSTSL 186
DB 133 IQKGQGTVACTWBERGRDTHLYTEYTLQLSGPKNLTWQKQCDYCDLDFGAINLTPSP 192
QY 187 QGKKYLVWVOAANALGMEESKQIHDIDIVIPSAVISRAETINATVPKTIYWDSQ 246
DB 193 E--SNFTAKYAVNSLSSSSSLPSTFTFLDIVRPLPPMDIRIKPKAKASVSRCTLYWRD 250
QY 247 TIEKYSCEMRKYATNTQTNVYKFPDNTFTYV--QOSEFYLEPNIKYVQVRCQ-ETGKRY 303
DB 251 LV--LNLRLRFRPSNSRLMM-----VNTKAKGRHDLDLKPFTEYEFQISSKHLKYG 304
QY 304 WQPMGSLFFHKTPEYV 320
DB 305 WDSGSLRQTPREBP 321

RESULT 3

US-08-915-495-2

Sequence 2, Application US/08915495

Patent No. 5852176

GENERAL INFORMATION:

APPLICANT: Gubler, Ulrich A

APPLICANT: Presky, David H

TITLE OF INVENTION: RECEPTORS FOR HUMAN IL-12

NUMBER OF SEQUENCES: 4

CORRESPONDENCE ADDRESS:

ADDRESSEE: Hoffmann-La Roche Inc.

STREET: 340 Kingeland Street